

25. An isolated nucleic acid molecule selected from the group consisting of:

- (a) a MEKK1 nucleic acid; and
- (b) an allelic variant thereof.

26. An isolated polypeptide molecule selected from the group consisting of:

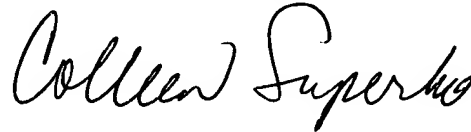
- (a) a MEKK1 polypeptide; and
- (b) an allelic variant thereof.

REMARKS

This Preliminary Amendment does not introduce new subject matter as support is found in the application filed.

No fees are believed to be due in connection with this correspondence. However, please charge any payments due or credit any overpayments to our Deposit Account No. 08-0219.

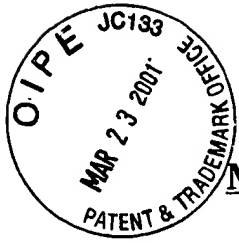
Respectfully submitted,
HALE AND DORR LLP



Colleen Superko
Reg. No. 39,850

Dated: March 21, 2001

HALE AND DORR LLP
60 State Street
Boston, MA 02109
Tel.: (617) 526-6564
Fax: (617) 526-5000



**MARKED-UP VERSION OF REPLACEMENT PARAGRAPHS IN
SPECIFICATION UNDER 37 C.F.R. §1.121(B)(1)**

ON PAGE 7, PARAGRAPH AT LINES 23-26:

Figure 2 depicts a summary of the alignment of the human MEKK1 protein (SEQ ID NO:2) with a partial human MEKK1 protein (GenBank Accession Number AF042838), (SEQ ID NO:3) rat MEKK1 (GenBank Accession Number U48596) (SEQ ID NO:4) , and mouse MEKK1 (GenBank Accession Number ~~117340~~). AF 117340.1) (SEQ ID NO:5).

ON PAGE 23, SUBPARAGRAPHS AT LINES 12-27:

a nucleic acid molecule comprising from about 10 to about 64 contiguous nucleotides from the nucleic acid sequence (SEQ ID NO:6)
ATGGCGGCGGCGGCGGGGAATCGCGCCTCGTCGGGATTCCCGGGCGCCA
GGGCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising from about 10 to about 64 contiguous nucleotides from the nucleic acid sequence (SEQ ID NO:7)
GAGAAAATGGCGGCGGCGGGGAATCGCGCCTCGTCGGGATTCCCGG
GCGCCAGGGCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:8) GCGCGCCCGCG and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:9) CCGCGAGCCGCGGCGGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

ON PAGE 24, SUBPARAGRAPHS AT LINES 10-30:

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:10)** TTTGGATGGTCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:11)** GGACAGCTTC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:12)** CCCCTGAGTGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:13)** GCCAGCATTT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:14)** CATCTAGACCT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:15)** GGCTGTAGCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:16)** GTAATGCTGT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

ON PAGE 25, SUBPARAGRAPH AT LINES 4-6:

a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:17)** GGATGCCCTCCCCAT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

ON PAGE 35, SUBPARAGRAPHS AT LINES 23-30:

a polypeptide comprising from about 5 to about 19 contiguous amino acids from the amino acid sequence **(SEQ ID NO:18)**

MAAAAGNRASSSGFPGARAT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising from about 5 to about 19 contiguous amino acids from the amino acid sequence (SEQ ID NO:19)

EKMAAAAGNRASSSGFPGARAT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

ON PAGE 36, SUBPARAGRAPHS AT LINES 1-24:

a polypeptide comprising the amino acid sequence (SEQ ID NO:20) SAPAA and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:21) ASRGG and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:22) CARGT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:23) VSSSTH and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:24) LMAIADE and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:25) TLDGQQDSFLQASVPNNYLETTENSSPECT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:26) LASISV and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence **(SEQ ID NO:27)** SFGCSSNSSNAVIPSDE and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2; or

a polypeptide comprising the amino acid sequence **(SEQ ID NO:28)** SQDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYREDT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2.

MARKED-UP VERSION OF AMENDED CLAIMS UNDER
37 C.F.R. § 1.121(b)(1)

Please amend claims 3 and 10 as described below. As required by 37 C.F.R. § 1.121(b)(1), the amended claims are rewritten with the amended claim language included. A marked-up version of the amended claims is attached to show the changes relative to the as-filed version.

3. (Once Amended) An isolated nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising from about 10 to about 64 contiguous nucleotides from the nucleic acid sequence **(SEQ ID NO:6)** ATGGCGGCGGCGGCGGGGAATCGCGCCTCGTCGGGATTCCCGGGCGCCA GGGCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(b) a nucleic acid molecule comprising from about 10 to about 64 contiguous nucleotides from the nucleic acid sequence **(SEQ ID NO:7)** GAGAAAATGGCGGCGGCGGGGAATCGCGCCTCGTCGGGATTCCCGG GCGCCAGGGCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(c) a nucleic acid molecule comprising the nucleic acid sequence **(SEQ ID NO:8)** GCGCGCCCGCG and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(d) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:9) CCGCGAGCCGCGGCGGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(e) a nucleic acid molecule comprising the nucleic acid sequence GCACGTGGA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(f) a nucleic acid molecule comprising the nucleic acid sequence CTACGTCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(g) a nucleic acid molecule comprising the nucleic acid sequence CCAGTTCCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(h) a nucleic acid molecule comprising the nucleic acid sequence GCTATTGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(i) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:10) TTTGGATGGTCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(j) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:11) GGACAGCTTC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(k) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:12) CCCCTGAGTGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(l) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:13) GCCAGCATTT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(m) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:14) CATCTAGACCT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(n) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:15) GGCTGTAGCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(o) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:16) GTAATGCTGT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(p) a nucleic acid molecule comprising the nucleic acid sequence CCCAGTGAC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

(q) a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:17) GGATGCCCTCCCCAT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1; and

(r) a nucleic acid molecule comprising the nucleic acid sequence GGCCTTTCG and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1.

10. (Once Amended) An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising from about 5 to about 19 contiguous amino acids from the amino acid sequence (SEQ ID NO:18) MAAAAGNRASSSGFPGARAT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

b) a polypeptide comprising from about 5 to about 19 contiguous amino acids from the amino acid sequence (SEQ ID NO:19) EKMAAAAGNRASSSGFPGARAT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

c) a polypeptide comprising the amino acid sequence (SEQ ID NO:20) SAPAA and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

d) a polypeptide comprising the amino acid sequence (SEQ ID NO:21) ASRGG and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

e) a polypeptide comprising the amino acid sequence (SEQ ID NO:22) CARGT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

f) a polypeptide comprising the amino acid sequence (SEQ ID NO:23) VSSSTH and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

g) a polypeptide comprising the amino acid sequence (SEQ ID NO:24) LMAIADE and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

h) a polypeptide comprising the amino acid sequence (SEQ ID NO:25) TLDGQQDSFLQASVPNNYLETTENSPECT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

i) a polypeptide comprising the amino acid sequence (SEQ ID NO:26) LASISV and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

j) a polypeptide comprising the amino acid sequence (SEQ ID NO:27) SFGCSSNSSNAVIPSDE and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2; and

k) a polypeptide comprising the amino acid sequence (SEQ ID NO:28) SQDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYREDT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2.